

1 GCGTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT
 51 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GAACTGGCTT
 101 CAGCAGAGCG CAGATACCAA ATACTGTCCT TCTAGTGTAG CCGTAGTTAG
 151 GCCACCACTT CAAGAACTCT GTAGCACCGC CTACATACCT CGCTCTGCTA
 201 ATCCTGTTAC CAGTGGCTGC TGCCAGTGGC GATAAGTCGT GTCTTACCGG
 251 GTTGGACTCA AGACGATAGT TACCGGATAA GGCGCAGCGG TCGGGCTGAA
 301 CGGGGGGTTT GTGCACACAG CCCAGCTTGG AGCGAACGAC CTACACCGAA
 351 CTGAGATACC TACAGCGTGA GCTATGAGAA AGCGCCACGC TTCCCGAAGG
 401 GAGAAAGGCG GACAGGTATC CGGTAAGCGG CAGGGTCGGA ACAGGAGAGC
 451 GCACGAGGGA GCTTCCAGGG GGAAACGCCT GGTATCTTTA TAGTCTGTG
 501 GGGTTTCGCC ACCTCTGACT TGAGCGTCGA TTTTGTGAT GCTCGTCAGG
 551 GGGGCGGAGC CTATGGAAAA ACGCCAGCAA CGCCGAATTA CCGCGGTCTT
 601 TCTCAACGTA ACACTTTACA GCGGCGCGTC ATTTGATATG ATGCGCCCCG
 651 CTTCCCGATA AGGGAGCAGG CCAGTAAAAG CATTACCCGT GGTGGGGTTC
 701 CCGAGCGGCC AAAGGGAGCA GACTCTAAAT CTGCCGTCAT CGACTTCGAA
 751 GGTTCAATC CTTCCCCAC CACCATCACT TTCAAAGTC CGAAAGAATC
 801 TGCTCCCTGC TTGTGTGTTG GAGGTCGCTG AGTAGTGGC GAGTAAAT
 851 TAAGCTACAA CAAGGCAAGG CTTGACCGAC AATTGCATGA AGAATCTGCT
 901 TAGGGTTAGG CGTTTTGCGC TGCTTCGCGA TGTACGGGCC AGATATACCG
 951 GTTGACATTG ATTATTGACT AGTTATTAAT AGTAATCAAT TACGGGGTCA
 1001 TTAGTTCATA GCCCATATAT GGAGTTCCGC GTTACATAAC TTACGGTAAA
 1051 TGGCCCGCCT GGCTGACCGC CCAACGACCC CCGCCCATTG ACGTCAATAA
 1101 TGACGTATGT TCCCATAGTA ACGCCAATAG GGACTTTCCA TTGACGTCAA
 1151 TGGGTGGACT ATTTACGGTA AACTGCCAC TTGGCAGTAC ATCAAGTGTA
 1201 TCATATGCCA AGTACGCCCC CTATTGACGT CAATGACGGT AAATGGCCCC
 1251 CCTGGCATTG TGCCAGTAC ATGACCTTAT GGGACTTTCC TACTTGGCAG
 1301 TACATCTACG TATTAGTCAT CGCTATTACC ATGGTGATGC GGTTTTGGCA
 1351 GTACATCAAT GGGCGTGGAT AGCGGTTTGA CTCACGGGGA TTTCCAAGTC
 1401 TCCACCCCAT TGACGTCAAT GGGAGTTTGT TTTGGCACCA AAATCAACGG
 1451 GACTTTCCAA AATGTCGTAA CAACTCCGCC CCATTGACGC AAATGGGCGG
 1501 AATTCCTGGG CGGGACTGGG GAGTGGCGAG CCCTCAGATG CTGCATATAA
 1551 GCAGCTGCTT TTTGCCTGTA CTGGGTCTCT CTGGTTAGAC CAGATCTGAG
 1601 CCTGGGAGCT CTCTGGCTAA CTAGAGAACC CACTGCTTAA GCCTCAATAA
 1651 AGCTTCTAGA GATCCCTCGA CCTCGAGGGA TCTTCATAC CTACCAGTTC

FIG. 1A

Out
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1701 TGGCCTGCA GGTCCGGCC GCGACTCTAG AGGATCTTG TGAAGGAACC
1751 TTA CTCTGT GGTGTGACAT AATTGGACAA ACTACCTACA GAGATTTAAA
1801 GCTCTAAGGT AAATATAAAA TTTTAAAGTG TATAATGTGT TAACTACTG
1851 ATTCTAATTG TTTGTGTATT TTAGATTCCA ACCTATGGAA CTGATGAATG
1901 GGAGCAGTGG TGAATGCCT TTAATGAGGA AAACCTGTTT TGCTCAGAAG
1951 AAATGCCATC TAGTGATGAT GAGGCTACTG CTGACTCTCA ACATTCTACT
2001 CCTCCAAAAA AGAAGAGAAA GGTAGAAGAC CCCAAGGACT TTCCTTCAGA
2051 ATTGCTAAGT TTTTGTAGTC ATGCTGTGTT TAGTAATAGA ACTCTTGCTT
2101 GCTTTGCTAT TTACACCACA AAGGAAAAAG CTGCACTGCT ATACAAGAAA
2151 ATTATGGAAA AATATTCTGT AACCTTTATA AGTAGGCATA ACAGTTATAA
2201 TCATAACATA CTGTTTTTTC TTA CTCCACA CAGGCATAGA GTGCTGCTA
2251 TTAATAACTA TGCTCAAAAA TTGTGTACCT TTAGCTTTTT AATTGTAAA
2301 GGGGTTAATA AGGAATATTT GATGTATAGT GCCTTGACTA GAGATCATAA
2351 TCAGCCATAC CACATTTGTA GAGGTTTTAC TTGCTTTAAA AAACCTCCCA
2401 CACCTCCCCC TGAACCTGAA ACATAAAATG AATGCAATTG TTGTTGTAA
2451 CTTGTTTATT GCAGCTTATA ATGGTTACAA ATAAAGCAAT AGCATCACAA
2501 ATTTACAAA TAAAGCATTT TTTTCACTGC ATTCTAGTTG TGGTTTGTCC
2551 AAATCATCA ATGTATCTTA TCATGTCTGG ATCCTGTGGA ATGTGTGTCA
2601 GTTAGGGTGT GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAAA
2651 GCATGCATCT CAATFAGTCA GCAACCAGGT GTGGAAAGTC CCCAGGCTCC
2701 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAT
2751 AGTCCCGCCC CTA ACTCCGC CCATCCCGCC CCTA ACTCCG CCCAGTCCG
2801 CCCATTCTCC GCCCCATGGC TGA CTAA TTTTATTTA TGCAGAGGCC
2851 GAGGCCGCCT CGGCCTCTGA GCTATTCCAG AAGTAGTGAG GAGGCTTTTT
2901 TGGAGGCCTA GGCTTTTGCA AAAAGCTAAT TC

FIG. 1B

CCTAAGATGAGCTTTCCATGTAAATTTGTAGCCAGCTTCCTTCTGATTTTCAATGTTTCT (60)
 METSERPHEPROCYSLYSPHEVALALASERPHELEULEULEPHEASNVALSER
 TCCAAAGGTGCAGTCTCCAAGAGATTACGAATGCCTTGGAAACCTGGGGTGCCTTGGGT (120)
 SERLYSGLYALAVALSERLYSGLUILETHRASNALALEUGLUTHRTRPGLYALALEUGLY
 20 CAGGACATCAACTTGGACATTCCTAGTTTTCAAATGAGTGATGATATTGACGATATAAAA (180)
 GLNASPILEASNLEUASPILEPROSERPHEGLNMETSERASPPASPILEASPASPILELYS
 TGGGAAAAAACTTCAGACAAGAAAAAGATTGCACAATTCAGAAAAGAGAAAGAGACTTTC (240)
 40 TRPGLULYSTHRSERASPLYSLYSILEALAGLNPHARGLYSGLULYSGLUTHRPH
 AAGGAAAAAGATACATATAAGCTATTTAAAAATGGAACCTCTGAAAATTAAGCATCTGAAG (300)
 60 LYSGLULYSASPTHRITYRLYSLEUPHELYSASNGLYTHRLEULYSILELYSHISLEULYS
 ---CHO---
 80 ACCGATGATCAGGATATCTACAAGGTATCAATATATGATACAAAAGGAAAAATGTGTTG (360)
 THRASPASPLNASPILETYRLYSVALSERILETYRASPTHRLYSGLYLYSASNVALLEU
 GAAAAAATAATTTGATTTGAAGATTCAAGAGAGGGTCTCAAAACCAAAGATCTCCTGGACT (420)
 100 GLULYSILEPHEASPLEULYSILEGLNGLUARGVALSERLYSPROLYSILESERTRPTHR
 TGTATCAACACAACCTGACCTGTGAGGTAAATGAATGGAACCTGACCCCGAATTAACCTG (480)
 120 CYSILEASNTHRTHRLEUTHRHCYSGLUVALMETASNGLYTHRASPPOGLULEUASNLEU
 ---CHO---
 TATCAAGATGGGAAACATCTAAAACCTTCTCAGAGGGTCATCACACAAGTGGACCAC (540)
 140 TYRGLNASPLGLYLYSHISLEULYSLEUSERGLNARGVALILETHRHSLYSTRPTHRTHR
 AGCCTGAGTGCAAAATTCAAGTGCACAGCAGGGAACAAAGTCAGCAAGGAATCCAGTGT (600)
 160 SERLEUSERALALYSPELYSCYSTHRLAGLYASNLYSVALSERLYSGLUSERSERVAL
 GAGCCTGTCACTGTCCAGAGAAAGGTCTGCACATCTATCTCATCTTGGCATATGTGGA (660)
 180 GLUPROVALSERCYSPOGLULYSGLYLEUASPILETYRLEUILEILEGLYILECYSGLY
 GGAGGCAGCCTCTTGATGGTCTTTGTGGCACTGCTCGTTTTCTATATCACAAAAGGAAA (720)
 200 GLYGLYSERLEULEUMETVALPHEVALALALEULEUVALPHETYRILETHRHSARGLYS
 ---TM---
 AAACAGAGGAGTCGGAGAAATGATGAGGAGCTGGAGACAAGAGCCCACAGAGTAGCTACT (780)
 220 LYSGLNARGSERARGARGASNASPLUGLULEUGLUTHRARGALAHISARGVALALATHR
 GAAGAAAGGGGCCGAAGCCCAACAAATTCAGCTTCAACCCCTCAGAATCCAGCAACT (840)
 240 GLUGLUARGGLYARGLYSPROGLNGLNILEPROALASERTHRPROGLNASNPROALATHR
 TCCCAACATCTCTCCACACCTGGTCACTGTTCCAGGCACCTAGTCACTCGTCCCCCG (900)
 260 SERGLNHISPROPROPROPROGLYHISARGSERGLNALAPROSERHISARGPROPRO
 CCTCTGGAACACCGTGTTCAAGCACCAGCCTCAGAAGAGGCTCTGCTCCGTCCGGGCACA (960)
 280 PROPROGLYHISARGVALGLNHISGLNPROGLNLYSARGPROPROALAPROSERGLYTHR

FIG. 2A

Conty
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300 CAAGTTCAC[^]CAGCAGAAAG[^]CCCCGCCCT[^]CCCCAGACCT[^]CGAGTTCAGC[^]AAAACCTCC[^] (1020)
GLNVALHISGLNGLNLYSGLYPROPROLEU[^]PROARGPROARGVALGLNPROLYSPROPRO
320 CATGGGGCAGCAGAA[^]ACTCATTGTCCCCT[^]CTCTAATTAAAAAGATAGAAACTGTCT[^] (1080)
HISGLYALAALAGLUASNSERLEUSERPRO[^]SERSERAS[^]END
TTTTCAATAAAAAGCACTGTGGATTTCTGCCCTCCTGATGTGCATATCCGTACTTCCATG (1140)
AGGTGTTTTCTGTGTGCAGAACATTGTCACTCCTGAGGCTGTGGGCCACAGCCACCTCT (1200)
GCATCTTCGAACTCAGCCATGTGGTCAACATCTGGAGTTTTTGGTCTCCTCAGAGAGCTC (1260)
CATCACACCAGTAAGGAGAAGCAATATAAGTGTGATTGCAAGAATGGTAGAGGACCGAGC (1320)
ACAGAAATCTTAGAGATTTCTTGTCCCCTCTCAGGTCATGTGTAGATGCCGATAAATCAAG (1380)
TGATTGGTGTGCCTGGGTCTCACTACAAGCAGCCTATCTGCTTAAGAGACTCTGGAGTTT (1440)
CTTATGTGCCCTGGTGGACACTTGCCACCATCCTGTGAGTAAAGTGAATAAAAGCTT (1500)
TGAC (1504)

FIG. 2B

1 GCGTAATCT GCTGCTTGCA AACAAAAAA CCACCGCTAC CAGCGGTGGT
51 TTGTTTGCCG GATCAAGAGC TACCAACTCT TTTTCCGAAG GTAAGTGGCT
101 TCAGCAGAGC GCAGATACCA AATACTGTCC TTCTAGTGTA GCCGTAGTTA
151 GGCCACCACT TCAAGAACTC TGTAGCACCG CCTACATACC TCGCTCTGCT
201 AATCCTGTTA CCAGTGGCTG CTGCCAGTGG CGATAAGTCG TGTCTTACCG
251 GGTGGACTC AAGACGATAG TTACCGGATA AGGCGCAGCG GTCGGGCTGA
301 ACGGGGGGTT CGTGCACACA GCCCAGCTTG GAGCGAACGA CCTACACCGA
351 ACTGAGATAC CTACAGCGTG AGCATTGAGA AAGCGCCACG CTTCCCGAAG
401 GGAGAAAGGC GGACAGGTAT CCGGTAAGCG GCAGGGTCGG AACAGGAGAG
451 CGCACGAGGG AGCTTCCAGG GGGAAACGCC TGGTATCTTT ATAGTCCTGT
501 CGGGTTTCGC CACCTCTGAC TTGAGCGTCG ATTTTGTGA TGCTCGTCAG
551 GGGGGCGGAG CCTATGGAAA AACGCCAGCA ACGCAAGCTA GCTTCTAGCT
601 AGAAATTGTA AACGTTAATA TTTTGTTAAA ATTCGCGTTA AATTTTGT
651 AAATCAGCTC ATTTTAAAC CAATAGGCCG AAATCGGCAA AATCCCTTAT
701 AAATCAAAAG AATAGCCCGA GATAGGGTTG AGTGTTGTTT CAGTTTGGAA
751 CAAGAGTCCA CTATTAAAGA ACGTGGACTC CAACGTCAA GGGCGAAAAA
801 CCGTCTATCA GGGCGATGGC CGCCCACTAC GTGAACCATC ACCCAAATCA
851 AGTTTTTTGG GGTGAGGTG CCGTAAAGCA CTAAATCGGA ACCCTAAAGG
901 GAGCCCCCGA TTTAGAGCTT GACGGGGAAA GCCGGCGAAC GTGGCGAGAA
951 AGGAAGGGAA GAAAGCGAAA GGAGCGGGCG CTAGGGCGCT GGCAAGTGTA
1001 GCGGTCACGC TGCGCGTAAC CACCACACC GCCGCGCTTA ATGCGCGCT
1051 ACAGGGCGCG TACTATGGTT GCTTTGACGA GCACGTATAA CGTGCTTTCC

FIG. 6A

1101 TCGTTGGAAT CAGAGCGGGA GCTAAACAGG AGGCCGATTA AAGGGATTTT
 1151 AGACAGGAAC GGTACGCCAG CTGGATCACC GCGGTCTTTC TCAACGTAAC
 1201 ACTTTACAGC GGCGCGTCAT TTGATATGAT GCGCCCCGCT TCCCCATAAG
 1251 GGAGCAGGCC AGTAAAAGCA TTACCCGTGG TGGGGTCCC GAGCGGCCAA
 1301 AGGGAGCAGA CTCTAAATCT GCCGTCATCG ACTTGAAGG TTCGAATCCT
 1351 TCCCCACCA CCATCACTTT CAAAAGTCCG AAAGAATCTG CTCCTGCTT
 1401 GTGTGTTGGA GGTCGCTGAG TAGTGCGCGA GTAAATTTA AGCTACAACA
 1451 AGGCAAGGCT TGACCGACAA TTGCATGAAG AATCTGCTTA GGGTTAGGCG
 1501 TTTTGGCTG CTTGCGGATG TACGGGCCAG ATATACGCGT TGACATTGAT
 1551 TATTGACTAG TTATTAATAG TAATCAATTA CGGGGTCATT AGTTCATAGC
 1601 CCATATATGG AGTTCCGCGT TACATAACTT ACGGTAAATG GCGCGCTGG
 1651 CTGACCGCCC AACGACCCCC GCCCATTGAC GTCAATAATG ACGTATGTTG
 1701 CCATAGTAAC GCCAATAGGG ACTTTCCATT GACGTCAATG GGTGGACTAT
 1751 TTACGGTAA CTGCCCACTT GGCAGTACAT CAAGTGTATC ATATGCCAAG
 1801 TACGCCCCCT ATTGACGTCA ATGACGGTAA ATGGCCCGCC TGGCATTATG
 1851 CCCAGTACAT GACCTTATGG GACTTTCCTA CTTGGCAGTA CATCTACGTA
 1901 TTAGTCATCG CTATTACCAT GGTGATGCGG TTTTGGCAGT ACATCAATGG
 1951 GCGTGGATAG CGGTTTGACT CACGGGGATT TCCAAGTCTC CACCCCATTG
 2001 ACGTCAATGG GAGTTTGTTT TGGCACCAA ATCAACGGGA CTTTCCAAAA
 2051 TGTGTAACA ACTCCGCCCC ATTGACGCAA ATGGCGGAA TTCCTGGGCG
 2101 GGA CTGGGGA GTGGCGAGCC CTCAGATGCT GCATATAAGC AGCTGCTTTT
 2151 TGCCTGTA CT GGGTCTCTCT GGTTAGACCA GATCTGAGCC TGGGAGCTCT
 2201 CTGGCTAACT AGAGAACCCA CTGCTTAAGC CTCAATAAAG CTTCTAGAGA
 2251 TCCCTCGACC TCGAGATCCA TTGTGCTGGC GCGGATTCTT TATCACTGAT

FIG. 6B

2301 AAGTTGGTGG ACATATTATG TTTATCAGTG ATAAAGTGTC AAGCATGACA
 2351 AAGTTGCAGC CGAATACAGT GATCCGTGCC GCCCTAGACC TGTTGAACGA
 2401 GGTCCGGCGTA GACGGTCTGA CGACACGCAA ACTGGCGGAA CGGTTGGGGG
 2451 TTCAGCAGCC GGCGCTTTAC TGGCACTTCA GGAACAAGCG GGCGCTGCTC
 2501 GACGCACTGG CCGAAGCCAT GCTGGCGGAG AATCATAGCA CTTCGGTGCC
 2551 GAGAGCCGAC GACGACTGGC GCTCATTTCT GACTGGGAAT GCGCGCAGCT
 2601 TCAGGCAGGC GCTGCTCGCC TACCGCCAGC ACAATGGATC TCGAGGGATC
 2651 TTCCATACCT ACCAGTTCTG CGCCTGCAGG TCGCGGCCGC GACTCTAGAG
 2701 GATCTTTGTG AAGGAACCTT ACTTCTGTGG TGTGACATAA TTGGACAAAC
 2751 TACCTACAGA GATTTAAAGC TCTAAGGTAA ATATAAAATT TTTAAGTGTA
 2801 TAATGTGTTA AACTACTGAT TCTAATTGTT TGTGTATTTT AGATTCCAAC
 2851 CTATGGAAC~~T~~GATGAATGGG AGCAGTGGTG GAATGCCTTT AATGAGGAAA
 2901 ACCTGTTTTG CTCAGAAGAA ATGCCATCTA GTGATGATGA GGCTACTGCT
 2951 GACTCTCAAC ATTCTACTCC TCCAAAAAAG AAGAGAAAGG TAGAAGACCC
 3001 CAAGGACTTT CCTTCAGAAT TGCTAAGTTT TTTGAGTCAT GCTGTGTTTA
 3051 GTAATAGAAC TCTTGCTTGC TTTGCTATTT ACACCACAAA GGAAAAAGCT
 3101 GCACTGCTAT ACAAGAAAAT TATGGAAAAA TATTCTGTAA CCTTTATAAG
 3151 TAGGCATAAC AGTTATAATC ATAACATACT GTTTTTTCTT ACTCCACACA
 3201 GGCATAGAGT GTCTGCTATT AATAACTATG CTCAAAAATT GTGTACCTTT
 3251 AGCTTTTTTAA TTTGTAAAGG GGTTAATAAG GAATATTTGA TGTATAGTGC
 3301 CTTGACTAGA GATCATAATC AGCCATACCA CATTTGTAGA GGTTTTACTT
 3351 GCTTTAAAAA ACCTCCCACA CCTCCCCCTG AACCTGAAAC ATAAAATGAA
 3401 TGCAATTGTT GTTGTTAACT TGTTTATTGC AGCTTATAAT GGTTACAAAT
 3451 AAAGCAATAG CATCACAAAT TTCACAAATA AAGCATTTTT TTTACTGCAT

FIG. 6C

3501 TCTAGTTGTG GTTTGTCCAA ACTCATCAAT GTATCTTATC ATGTCTGGAT
3551 CCTGTGGAAT GTGTGTCAGT TAGGGTGTGG AAAGTCCCCA GGCTCCCCAG
3601 CAGGCAGAAG TATGCAAAGC ATGCATCTCA ATTAGTCAGC AACCAGGTGT
3651 GGAAAGTCCC CAGGCTCCCC AGCAGGCAGA AGTATGCAAA GCATGCATCT
3701 CAATTAGTCA GCAACCATAG TCCCGCCCCT AACTCCGCCC ATCCCGCCCC
3751 TAACTCCGCC CAGTTCCGCC CATTCTCCGC CCCATGGCTG ACTAATTTTT
3801 TTTATTTATG CAGAGGCCGA GGCCGCCTCG GCCTCTGAGC TATTCCAGAA
3851 GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG CTTTGTGAAA AAGCTAATTC

FIG. 6D

AGACTCTCAGGCCTTGGCAGGTGCGTCTTTCAGTTCCTCCCTCACACTTCGGGTTCCTCGG (60)
 GAGGAGGGGCTGGAACCCTAGCCCATCGTCAGGACAAAGATGCTCAGGCTGCTCTTGGCT (120)
 CTCAACTTATTCCTTCAATTCAAGTAACAGGAAACAAGATTTTGGTGAAGCAGTCGCC (180)
 LEUASNLEUPHEPROSERILEGLNVALTHRGLYASNLYSILELEUVALLYSLNSERPRO
 ATGCTTGTAGCGTACGACAATGCGGTCAACCTTAGCTGCAAGTATTCCTACAATCTCTT (240)
 METLEUVALALATYRASPASNALAVASNLEUSERCYSLYSTYRSERTYRASNLEUPHE
 TCAAGGGAGTTCGGGCATCCCTTACAAAGGACTGGATAGTGCTGTGGAGTCTGTGT (300)
 SERARGGLUPHEARGALASERLEUHSLSGLYLEUASPSEALAVAGLUVALCYSVAL
 GTATATGGGAATTACTCCCAGCAGCTTCAGGTTTACTCAAAAACGGGGTTCAGTGTGAT (360)
 VALTYRGLYASNTYRSEGLNGLNLEUGLNVALTYRSELYSTHRLYPHEASNCYSASP
 GGGAAATTGGGCAATGAATCAGTGACATTCTACCTCCAGATTTGTATGTTAACCAACA (420)
 GLYLYSLEUGLYASNGLUSERVALTHRPHETYLEUGLNASNLEUTYRVALASNGLNTHR
 GATATTTACTTCTGCAAAATTGAAGTTATGTATCCTCCTCCTACCTAGACAATGAGAAG (480)
 ASPILETYRPHECYSLYSILEGLUVALMETTYRPROPROTYRLEUASPASNGLULYS
 AGCAATGGAACCATTATCCATGTGAAAGGAAACACCTTTGTCCAAGTCCCCTATTTCC (540)
 SERASNGLYTHRILEILEHISVALLYSLYLYSHISLEUCYSPROSERPROLEUPHEPRO
 GGACCTTCTAAGCCCTTTTGGGTGCTGGTGGTGGTGGTGGAGTCTGGCTTGCTATAGC (600)
 GLYPROSERLYSPROPHETRPVALLEUVALVALGLYGLYVALLEUALACYSYRSE
 TTGCTAGTAACAGTGGCCTTTATTATTTCTGGGTGAGGAGTAAGAGGAGCAGGCTCTG (660)
 LEULEUVALTHRVALALAPHEILEILEPHETRPVALARGSERLYSARGSERARGLEULEU
 CACAGTGACTACATGAACATGACTCCCCGCCGCCCGGGCCACCCGCAAGCATTACCAG (720)
 HISSERASPTYRMETASNMETTHRPROARGARGPROGLYPROTHRARGLYSHISTYRGLN
 CCCTATGCCCCACCACGCGACTTCGCAGCCTATCGCTCCTGACACGGACGCCTATCCAG (780)
 PROTYRALAPROPROARGASPPHEALAALATYRARGSEREND
 AGCCAGCCGGCTGGCAGCCCCCATCTGCTCAATATCACTGCTCTGGATAGGAAATGACC (840)
 CCATCTCCAGCCGGCCACCTCAGCCCTGTGGGCCACCAATGCCAATTTTCTCGAGTG (900)
 ACTAGACCAATATCAAGATCATTTTGAGACTCTGAAATGAAGTAAAGAGATTTCTGT (960)
 GACAGGCCAAGTCTTACAGTGCCATGGCCACATTCCAACCTACCATGTACTTAGTGACT (1020)
 TGACTGAGAAGTTAGGGTAGAAAACAAAAGGGAGTGGATTCTGGGAGCCTCTTCCCTT (1080)

FIG. 7A

CTCACTCACCTGCACATCTCAGTCAAGCAAAGTGTGGTATCCACAGACATTTTAGTTGCA (1140)
GAAGAAAGGCTAGGAAATCATTCCCTTTTGGTTAAATGGGTGTTAATCTTTGGTTAGTG (1200)
GGTTAAACGGGGTAAGTTAGAGTAGGGGAGGGATAGGAAGACATATTAAAAACCATT (1260)
AAACACTGTCTCCCACTCATGAAATGAGCCACGTAGTTCCTATTTAATGCTGTTTTCTT (1320)
TAGTTTAAATACATAGACATTGTCTTTTATGAATTCTGATCATTTTAGTCATTTTGA (1380)
CCAAATGAGGGATTTGGTCAAATGAGGGAATCCCTCAAAGCAATATCAGGTAAACCAAGT (1440)
TGCTTTCCTCACTCCCTGTATGAGACTTCAGTGTTAATGTTACAATATACTTTGAAA (1500)
GAATAAAATAGTTC (1514)

FIG. 7B

TAGACCCAGAGAGGCTCAGCTGCACTCGCCCGGCTGGGAGAGCTGGGTGTGGGGAACATG (60)
 MET
 GCCGGGCTCCGAGGCTCCTGCTGCTGCCCTGCTTCTGGCGCTGGCTCGCGGCTGCCT (120)
 ALAGLYPROPROARGLEULEULEULEUPROLEULEULEUALALEUALAARGGLYLEUPRO
 GGGGCCCTGGCTGCCAAGGTAAGAGCTTCCCAGGCTCTCCATGGCCACAGCTCCGGAGC (180)
 GLYALALEUALAALAGLN /
 TCTCCCTGCCCATGAGCTCAGAGCCCCAGTCTGAGCCACAGCACAGCCCCAGGAAGC (240)
 GGGTGGGTGCTGAGCGGCTCCAGTGTCTGAGGACTCAITTAAGAGAAGGAAAAAGGT (300)
 GGACCCGGTGGGAGTGGCCGGGGCTGTCCAGGCAGGGCCGCTGCTTTGGGAGGAAGAAG (360)
 CCCACAGTCTCGGAACAGGAGACAGCACCTCCCCAACACCACAGCCGGTCCCCAGATC (420)
 TGCTCCATGCCCGTAAGGCACCGTGTCTTTGGCGACATGTCAGCCCTGGGCTGTCTAG (480)
 GGCCCCACCATCCCCACCACTGTCCCCTGCAGGGAGGACATTCTGTCTTCTGGCCAG (540)
 ACTGATGGTGACAGCCCAGGTCTCCAGAGGTGCAGCAGTCTCCCCTGCACGACTGT (600)
 GLUVALGLNGLNSERPROHISCYSTHRTHRVA
 CCCCCTGGGAGCCTCCGTCAACATCACCTGCTCCACCAGCGGGGGCTGCGTGGGATCTA (660)
 LPROVALGLYALASERVALASNILETHRCYSSERTHRSEGLYGLYLEUARGGLYLETY
 ---CHO---
 CCTGAGGCACTCGGGCCACAGCCCAAGACATATTTACTACGAGGACGGGTGGTGCC (720)
 RLEUARGGLNLEUGLYPROGLNPROGLNASPILEILETYRTYRGLUASPGLYVALVALPR
 CACTACGGAACAGACGGTTCGGGGCCGCACTGACTTCTCAGGGTCCCAGGACAACCTGAC (780)
 OTHRTHRASPARGARGPHEARGGLYARGILEASPPHESERGLYSERGLNASPASNLEUTH
 ---CHO---
 TATCACCATGCACCGCTGCAGCTGTCCGACTGGCACCTACACCTGCCAGGCCATCAC (840)
 RILETHRMETHISARGLEUGLNLEUSERASPTHRLYTHRTYRTHRCYSLNALAILETH
 -
 GGAGGTCAATGTCTACGGCTCCGGCACCCCTGGTCTGGTGACAGAGGAAAGTCCCAAGG (900)
 RGLUVALASNVALTYRGLYSERGLYTHRLEUVALLEUVALTHRGLUGLUGLNSERGLNGL
 ATGGCACAGATGCTCGGACGCCCCACCAAGGGCTCTGCCCTCCCTGCCCCACCGACAGG (960)
 YTRPHISARGCYSSERASPALAPROPROARGALASERALEUPROALAPROPROTHRGL
 CTCCGCCCTCCCTGACCCGACAGACAGCCTCTGCCCTCCCTGACCCGCCAGCAGCCTCTGC (1020)
 YSERALEUPROASPPROGLNTHRALASERALEUPROASPPOPROALALASERALE
 CCTCCCTGCGGCCCTGGCGGTGATCTCCTCCTCCTCGGCTGGGCTGGGGGTGGCGTG (1080)
 ALEUPROALALEUALAVALILESERPHEULEUGLYLEUGLYLEUALALACY
 -----TM-----*

FIG. 8A

TGTGCTGGCGAGGACACAGATAAAGAACTGTGCTCGTGGCGGGATAAGAATTCGGCGGC (1140)
 SVALLEUALAARGTHRGLNILELYSLYSLEUCYSSERTRPARGASPLYSASNSERALAAL

 ATGTGTGGTGTACGAGGACATGTCCACAGCCGCTGCAACACGCTGTCTCCCCCAACCA (1200)
 ACYSVALVALTYRGLUASP⁴⁴METSERHISSE⁴⁵RARGCYSASNTHRLEUSERSERPROASNGL
 GTACCAGTGACCCAGTGGGCCCCTGCACGTCCCGCCTGTGGTCCCCCAACACCTTCCCT (1260)
 NTYRGLNEND
 GCCCCACCATGCCCCCACCCCTGCCACACCCCTCACCTGCTGTCCTCCCACGGCTGCA (1320)
 CAGAGTTTGAGGGGCCAGCGGTGCCAGCTCCAAGCAGACACACAGGCAGTGGCCAGGC (1380)
 CCCACGGTGCTTCTCAGTGGACAATGATGCCTCCTCCGGGAAGCCTTCCCTGCCAGCCC (1440)
 ACGCCGCCACCGGGAGGAAGCCTGACTGTCTTTGGCTGCATCTCCCGACCATGGCCAAG (1500)
 GAGGGCTTTTCTGTGGGATGGGCCTGGCA⁴⁶CGGCCCTCTCCTGTCA⁴⁷GTGCCGGCCAC⁴⁸C (1560)
 CACCAGCAGCCCCCAACCC⁴⁹CAGGCAGCCCGGCAGAGGACGGGAGGAGACCA⁵⁰GTCCCC⁵¹C (1620)
 ACCCAGCCGTACCAGAAATAAAGGCTTCTGTGCTTCAAAAAAAAA (1665)

FIG. 8B

CCCAAATGTCTCAGAATGTATGTCCAGAAACCTGTGGCTGCTTCAACCATTGACAGTTT (60)
 METSERGLNASNVALCYSPROARGASNLEUTRPLEULEUGLNPROLEUTHRVALL
 -29
 TGCTGCTGCTGGCTTCTGCAGACAGTCAAGCTGCAGCTCCCCAAAGGCTGTGCTGAAAC (120)
 EULEULEULEUALASERALAASPSEGLNALAALAALAPROPROLYSALAVALLEULYS
 -1 +1
 TTGAGCCCCCGTGGATCAACGTGCTCCAGGAGGACTCTGTGACTCTGACATGCCAGGGGG (180)
 10 EUGLUPROPROTRPILEASNVALLEUGLNGLUASPSERVALTHRLEUTHRCYSGNLGLYA
 *
 CTCGCAGCCCTGAGAGCGACTCCATTCACTGGTTCACAATGGGAATCTCATTCCCACC (240)
 30 LAARGSERPROGLUSERASPSEILEGLNTRPPHEHISASNGLYASNLEUILEPROTHR
 *
 ACACGCAGCCAGCTACAGGTTCAAGGCCACAACAATGACAGCGGGGAGTACACGTGCC (300)
 50 ISTHRGLNPROSERTYRARGPHELYSALAASNASNASNASPSEGLYGLUTYRTHRCYS
 ---CHO---
 *
 AGACTGGCCAGACCAGCCTCAGCGACCCTGTGCATCTGACTGTGCTTTCCGAATGGCTGG (360)
 70 LNTHRGlyGLNTHRSERLEUSERASPPROVALHISLEUTHRVALLEUSERGLUTRPLEUV
 *
 TGCTCCAGACCCCTCACCTGGAGTTCCAGGAGGGAGAAACCATCATGCTGAGGTGCCACA (420)
 90 ALLEUGLNTHRPROHISLEUGLUPHEGLNGLUGLYGLUTHRIEMETLEUARGCYSHISS
 *
 GCTGGAAGGACAAGCCTCTGGTCAAGGTCAATTCTTCCAGAATGGAAAATCCCAGAAAT (480)
 110 ERTPLYSASPLYSPOLEUVALLYSVALTHRPHEPHEGLNASNGLYLYSSERGLNLYSP
 *
 TCTCCGTTTGGATCCACCTTCTCCATCCACAAGCAAACCACAGTCAAGTGGTGATT (540)
 130 HESERARGLEUASPPROTHRPHESEILEPROGLNALAASNHISSEHISSEGLYASPT
 ---CHO---
 *
 ACCACTGCAACAGGAAACATAGGCTACAGCTGTTCTCATCCAAGCCTGTGACCATCACTG (600)
 150 YRHISCYSTHRGLYASNILEGLYTYRTHRLEUPHESESERLYSPROVALTHRIETHRV
 *
 TCCAAGTGCCACCATGGGACAGCTCTTCAACCAATGGGATCATTGTGGCTGTGGTCATTG (660)
 170 ALGLNVALPROSERMETGLYSERSESERPROMETGLYILEILEVALALAVALLILEA
 *
 CGACTGCTGTAGCAGCCATTGTTGCTGCTGTAGTGGCCTTGATCTACTGCAGGAAAAAGC (720)
 190 LATHRALAVALALAALAILEVALALAALAVALVALALEUILEYRCYSARGLYSLYSA
 -----TM-----
 *
 GGATTTGAGCCAATTCACCTGATCCTGTGAAGGCTGCCAATTTGAGCCACCTGGACGTC (780)
 210 RGILESERALAASNSETRHASPPOVALLYSALAALAGLNPHEGLUPROPROGLYARGG
 *
 AAATGATTGCCATCAGAAAGAGACAACCTGAAGAAACCAACAATGACTATGAAACAGCTG (840)
 230 LNMETILEALAILEARGLYSARGGLNLEUGLUGLUTHRASNASNASPTYRGLUTHRALAA
 *
 ACGGCGGCTACATGACTCTGAACCCAGGGCACCTACTGACGATGATAAAAACATCTACC (900)
 250 SPGLYGLYTYRMETTHRLEUASNPROARGALAPROTHRASPPASPLYSASNILETYRL

FIG. 9-A

270 TGA²⁸²CTTCCTCCCAACGACCATGTCAACAGTAATAACTAAAGAGTAACGTTATGCCATG (960)
 EUTHRLEUPROPROASNAPHISVALASN²⁸²SERASNEN²⁸²D
 TGGTCATACTCTCAGCTTGCTGAGTGGATGACAAAAAGAGGGGAATTGTTAAAGGAAAAT (1020)
 TTAAATGGAGACTGGAAAAATCCTGAGCAACAAAACCACTGGCCCTTAGAAATAGCTT (1080)
 TAACTTTGCTTAAACTACAACACAAGCAAACTTCACGGGGTCATACTACATACAAGCA (1140)
 TAAGCAAACTTAACTTGGATCATTCTGGTAAATGCTTATGTTAGAAATAAGACAACCC (1200)
 CAGCCAATCACAAGCAGCCTACTAACATAATAATTAGGTGACTAGGGACTTTCTAAGAAGA (1260)
 TACCTACCCCAAAAAACAATTATGTAATTGAAAACCAACCGATTGCCTTTATTTTGCTT (1320)
 CCACATTTTCCAATAAATACTTGCCTGTGACATTTTGCCACTGGAACAATAA²⁸²CTTCAT (1380)
 GAATTGCGCTCAGATTTTCTTTAACATCTTTTTTTTTTTGACAGAGTCTCAATCTG (1440)
 TTACCCAGGCTGGAGTGCAGTGGTGTATCTTGGCTCACTGCAAACCCGCTCCCAGGT (1500)
 TAAGCGATTCTCATGCCTCAGCCTCCAGTAGCTGGGATTAGAGGCATGTGCCATCATACT (1560)
 CCAGCTAATTTTGTATT²⁸²TTATTTTTTTTTTTAGTAGAGACAGGGTTTCGCAATGTT (1620)
 GGCCAGGCCGATCTCGAATCTGGCCTCTAGCGATCTGCCCCCTCGGCTCCCAAAGT (1680)
 GCTGGGATGACCAGCATCAGCCCCAATGTCCAGCCTCTTTAACATCTTCTTCTCTATGCC (1740)
 CTCTCTGTGGATCCCTACTGCTGGTTTCTGCCTTCTCAATGCTGAGAACA²⁸²AAATCACCTA (1800)
 TTCACTGCTTATGCAGTCGGAAGCTCCAGAAGAACAAGAGCCCAATTAACGAGACCACA (1860)
 TTAAGTCTCATTGTTTTGCCTTGGGATTGAGAAGAGAATTAGAGAGGTGAGGATCTGG (1920)
 TATTTCTGGACTAAATTCCCCTTGGGAAGACGAAGGGATGCTGCAGTTCCAAAAGAGA (1980)
 AGGACTCTTCAGAGTCATCTACCTGAGTCCCAAAGCTCCTGTCTGAAGCCACAGAC (2040)
 AATATGGTCCCAAATGACTGACTGCACCTTCTGTGCCTCAGCCGTTCTTGACATCAAGAA (2100)
 TCTTCTGTTCCACATCCACAAGCCAATAAATTAGTCAAACTGTTATTAACAGATG (2160)
 TAGCAACATGAGAAACGCTTATGTTACAGGTACATGAGAGCAATCATGTAAGTCTATA (2220)
 GACTTCAGAAATGTTAAAATAGACTAACCTCTAACAACAATTAAAGTGATTGTTTCAA (2280)
 GGTGAAAAA (2290)

FIG. 9-B

1 CTCAGCCTCGCTATGGCTCCCAGCAGCCCCCGCGCTGCCCGCCTCTGGTCCTGCTCGGGGCTCTGTTCCTCCCA
MetAlaProSerSerProArgProAlaLeuProAlaLeuLeuValLeuLeuGlyAlaLeuPhePro
(-25)
GGACCTGGCAATGCCCCAGACATCTGTGTCTCCCTCAAAAGTC
GlyProGlyAsnAlaGlnThrSerValSerProSerLysVal
(+11)
121 ATCTGTCCCGGGAGGCTCCGTGCTGGTGACATGCAGCACCTCTCTGTGACCAGCCCCAAGTTGTTGGGCATAGAGACC
IleLeuProArgGlyGlySerValLeuValThrCysSerThrSerCysAspGlnProLysLeuLeuGlyIleGluThr
(+1)
CCGTTGCCTAAAAAGGAGTTGCTCTCTGCTGCTGGGAACAACCGG
ProLeuProLysLysGluLeuLeuLeuProGlyAsnAsnArg
(+81)
241 AAGGTGTATGAAGTGAAGCAATGTGCAAGAAAGATAGCCAAACCAATGTGCTATTCAAACCTGCCCTGATGGGCAGTCAACA
LysValTyrGluLeuSerAsnValGlnGluAspSerGlnProMetCysTyrSerAsnCysProAspGlyGlnSerThr
GCTAAACACCTTCCTCACCGTGTACTGGACTCCAGAACGGGTG
AlaLysThrPheLeuThrValTyrTrpThrProGluArgVal
(+91)
361 GAACTGGCACCCCTCCCTCTCTTGGCAGCCAGTGGGCAAGAACCTTACCCTACGCTGCCAGGTGGAGGGTGGGCACCC
GluLeuAlaProLeuProSerTrpGlnProValGlyLysAsnLeuThrLeuArgCysGlnValGluGlyGlyAlaPro
---CHO---
CGGGCCAAACCTCACCGTGGTGCTGCTCCGTGGGAGAGAAGAG
ArgAlaAsnLeuThrValValLeuLeuArgGlyGluLysGlu
-----(+131)
481 CTGAAACGGGAGCCAGCTGTGGGGAGCCCGCTGAGGTACGACCACCGGTGCTGTGAGGAGAGATCACCATGGAGCC
LeuLysArgGluProAlaValGlyGluProAlaGluValThrThrValLeuValArgArgAspHisGlyAla
AATTTCTGTGCCGCACTGAACTGGACCTGCGGCCCCCAAGGG
AsnPheSerCysArgThrGluLeuAspLeuArgProGlnGly
---CHO---(+171)
601 CTGGAGCTGTTTGAGAACACCTCGGCCCCCTACCAGCTCCAGACCTTGTCTGTCAGCGACTCCCCCACAACCTTGTC
LeuGluLeuPheGluAsnThrSerAlaProTyrGlnLeuGlnThrPheValLeuProAlaThrProProGlnLeuVal
---CHO---
AGCCCCCGGCTCCTAGAGGTGGACACGACGGGACCGTGGTC
SerProArgValLeuGluValAspThrGlnGlyThrValVal
(+211)

FIG. 11-A

721 TGTTCCTGGACGGGCTGTTCCAGTCTCGGAGGCCAGGTCCACCTGGCAGTGGGGGACCAGAGGTTGAACCCACACA
 CysSerLeuAspGlyLeuPheProValSerGluAlaGlnValHisLeuAlaLeuGlyAspGlnArgLeuAsnProThr
 GTCACCTATGGCAACGACTCCTTCTCGGCCAAGGCCCTCAGTC
 ValThrTyrGlyAsnAspSerPheSerAlaLysAlaSerVal
 (+251)
 ---CHO---
 841 AGTGTGACCGCAGAGGACGAGGGCACCCAGCGGCTGACGTGTGCAGTAATACTGGGGAACCCAGAGCCAGGAGACACTG
 SerValThrAlaGluAspGluGlyThrGlnArgLeuThrCysAlaValIleLeuGlyAsnGlnSerGlnGluThrLeu
 ---CHO---
 CAGACAGTGACCATCTACAGCTTTCGGGCGCCCAACGTGATT
 GlnThrValThrIleTyrSerPheProAlaProAsnValIle
 (+291)
 961 CTGACGAAGCCAGAGGTCTCAGAAAGGACCGAGGTGACAGTGAAGTGTGAGGCCACCCTAGAGCCAAAGGTGACGCTG
 LeuThrLysProGluValSerGluGlyThrGluValThrValLysCysGluAlaHisProArgAlaLysValThrLeu
 AATGGGTTCCAGCCAGCCACTGGGCCCGAGGGCCCCAGCTC
 AsnGlyValProAlaGlnProLeuGlyProArgAlaGlnLeu
 (+331)
 1081 CTGCTGAAGGCCACCCAGAGGACAAACGGCGCAGCTTCTCCTGCTCTGCAACCCTGGAGGTGGCCGGCCAGCTTATA
 LeuLeuLysAlaThrProGluAspAsnGlyArgSerPheSerCysSerAlaThrLeuGluValAlaGlyGlnLeuIle
 CACAAGAACCAGACCCGGAGCTTCGTGCTCTGTATGGCCCC
 HisLysAsnGlnThrArgGluLeuArgValLeuTyrGlyPro
 (+371)
 ---CHO---
 1201 CGACTGGACGAGGGGATTGTCCGGGAAACTGGACGTGGCCAGAAATTCCCGACAGACTCCAATGTGCCAGGCTTGG
 ArgLeuAspGluArgAspCysProGlyAsnTrpThrTrpProGluAsnSerGlnThrProMetCysGlnAlaTrp
 ---CHO---
 GGGAAACCCATTGCCCCGAGCTCAAGTGTCTAAAGGATGGCACT
 GlyAsnProLeuProGluLeuLysCysLeuLysAspGlyThr
 (+411)
 1321 TTCCCACTGCCCATCGGGGAATCAGTGACTGTCACTCGAGATCTTGAGGGCACCTACCTCTGTGGGCCAGGAGCACT
 PheProLeuProIleGlyGluSerValThrValThrArgAspLeuGluGlyThrTyrLeuCysArgAlaArgSerThr
 CAAGGGAGGTCAACCCCGGAGGTGACCGTGAATGTGCTCTCC
 GlnGlyGluValThrArgGluValThrValAsnValLeuSer
 (+451)

FIG. 11-B


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1441 CCCCGGTATGAGATTGTTCATCATCTGTGGTAGCAGCCGCGAGTCATAATGGGCACTGCAGGCCTCAGCACGTACCTC
ProArgTyrGluIleValIleIleThrValAlaAlaAlaValIleMetGlyThrAlaGlyLeuSerThrTyrLeu
-----TM-----
TATAACCGCCAGCGGAAGATCAAGAAATACAGACTACAACAG
TyrAsnArgGlnArgLysIleLysLysTyrArgLeuGlnGln
(+491)
1561 GCGGCTTCCCATATTGGTGGCAGTGGTGCCACACTGAACACA
AlaGlnLysGlyThrProMetLysProAsnThrGlnAlaThrProPro
(+507)
CGGCTTCCCATATTGGTGGCAGTGGTGCCACACTGAACACA
GTGGAAGACATATGCCATGCAGCTACACCTACCGGCCCTGGGACGCCGGAGGACAGGGCATTGTCCTCAGTCAGATAC
1681 GGCACGCACTCTGATCTGTAGTCACATGACTAAGCCAAAGAGGAAGG
1801 AACAGCAATTGGGGCCCATGGTACCTGCACACCTAAACACTA

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FIG. 11-C

1 ..GGAGAGTC TGACCACCAT GCCACCTCCT CGCCTCCTCT TCTTCCTCCT
 51 CTTCTCACC CCCATGGAAG TCAGGCCCGA GGAACCTCTA GTGGTGAAGG
 101 TGAAGAGGG AGATAACGCT GTGCTGCAGT GCCTCAAGGG GACCTCAGAT
 151 GGGCCCACTC AGCAGCTGAC CTGGTCTCGG GAGTCCCCGC TTAAACCCTT
 201 CTTAAAACTC AGCCTGGGGC TGCCAGGCCT GGAATCCAC ATGAGGCCCC
 251 TGGCCATCTG GCTTTTCATC TTCAACGTCT CTCAACAGAT GGGGGGCTTC
 301 TACCTGTGCC AGCCGGGGCC CCCCTCTGAG AAGGCCTGGC AGCCTGGCTG
 351 GACAGTCAAT GTGGAGGGCA GCGGGGAGCT GTTCCGGTGG AATGTTTCGG
 401 ACCTAGGTGG CCTGGGCTGT GGCCTGAAGA ACAGTCCTC AGAGGGCCCC
 451 AGCTCCCCCT CCGGAAGCT CATGAGCCCC AAGCTGTATG TGTGGGCCAA
 501 AGACCGCCCT GAGATCTGGG AGGGAGAGCC TCCGTGTGTC CCACCGAGGG
 551 ACAGCCTGAA CCAGAGCCTC AGCCAGGACC TCACCATGGC CCCTGGCTCC
 601 ACACTCTGGC TGTCTGTGG GGTACCCCT GACTCTGTGT CCAGGGCCCC
 651 CCTCTCCTGG ACCCATGTGC ACCCAAGGG GCCTAAGTCA TTGCTGAGCC
 701 TAGAGCTGAA GGACGATCGC CCGGCCAGAG ATATGTGGGT AATGGAGACG
 751 GGTCTGTTGT TGCCCCGGGC CACAGCTCAA GACGCTGGAA AGTATTATTG
 801 TCACCGTGGC AACCTGACCA TGTCATTCCA CCTGGAGATC ACTGCTCGGC
 851 CAGTACTATG GCACTGGCTG CTGAGGACTG GTGGCTGGAA GGTCTCAGCT
 901 GTGACTTTGG CTTATCTGAT CTTCTGCCTG TGTTCCCTTG TGGGCATTCT
 951 TCATCTTCAA AGAGCCCTGG TCCTGAGGAG GAAAAGAAAG CGAATGACTG
 1001 ACCCCACCAG GAGATTCTTC AAAGTGACGC CTCCCCAGG AAGCGGGCCC
 1051 CAGAACCAGT ACGGGAACGT GCTGTCTCTC CCCACACCCA CCTCAGGCCT
 1101 CGGACGCGCC CAGCGTTGGG CCGCAGGCCT GGGGGGCACT GCCCCGTCTT
 1151 ATGGAAACCC GAGCAGCGAC GTCCAGGCGG ATGGAGCCTT GGGTCCCGG

FIG. 12-A

1201 AGCCGCCGGG AGTGGGCCCC GAAGAAGAGG AAGGGGAGGG CTATGAGGAA
1251 CCTGACAGTG AGGAGGACTC CGAGTTCTAT GAGAACGACT CCAACCTTGG
1301 GCAGGACCAG CTCTCCCAGG ATGGCAGCGG CTACGAGAAC CCTGAGGATG
1351 AGCCCCTGGG TCCTGAGGAT GAAGACTCCT TCTCCAACGC TGAGTCTTAT
1401 GAGAACGAGG ATGAAGAGCT GACCCAGCCG GTCGCCAGGA CAATGGACTT
1451 CCTGAGCCCT CATGGGTCAG CCTGGGACCC CAGCCGGGAA GCAACCTCCC
1501 TGGGGTCCCA GTCCTATGAG GATATGAGAG GAATCCTGTA TGCAGCCCCC
1551 CAGCTCCGCT CCATTTCGGG CCAGCCTGGA CCCAATCATG AGGAAGATGC
1601 AACTCTTAT GAGAACATGG ATAATCCCGA TGGGCCAGAC CCAGCCTGGG
1651 GAGGAGGGGG CCGCATGGGC ACCTGGAGCA CCAGGTGATC CTCAGGTGGC
1701 CAGCCTGGAT CTCCTCAAGT CCCCAAGATT CACACCTGAC TCTGAAATCT
1751 GAAGACCTCG AGCAGATGAT GCCAACCTCT GGAGCAATGT TGCTTAGGAT
1801 GTGTGCATGT GTGTAAGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT
1851 ATACATGCCA GTGACACTTC CAGTCCCCTT TGTATTCCTT AAATAAACTC
1901 AATGAGCTCT TCCAAAAAAA AAAA

FIG. 12-B

1 ACAAAGACAA ACTGCACCCA CTGAACTCCG CAGCTAGCAT CCAAATCAGC
51 CCTTGAGATT TGAGGCCTTG GAGACTCAGG AGTTTTGAGA GCAAAATGAC
101 AACACCCAGA AATTCAGTAA ATGGGACTTT CCCGGCAGAG CCAATGAAAG
151 GCCCTATTGC TATGCAATCT GGTCCAAAAC CACTCTTCAG GAGGATGTCT
201 TCACTGGTGG GCCCCACGCA AAGCTTCTTC ATGAGGGAAT CTAAGACTTT
251 GGGGGCTGTC CAGATTATGA ATGGGCTCTT CCACATTGCC CTGGGGGGTC
301 TTCTGATGAT CCCAGCAGGG ATCTATGCAC CCATCTGTGT GACTGTGTGG
351 TACCCTCTCT GGGGAGGCAT TATGTATATT ATTTCCGGAT CACTCCTGGC
401 AGCAACGGAG AAAAATCCA GGAAGTGTTT GGTCAAAGGA AAAATGATAA
451 TGAATTCATT GAGCCTCTTT GCTGCCATTT CTGGAATGAT TCTTTCAATC
501 ATGGACATAC TTAATATTAA AATTTCCCAT TTTTAAAAA TGGAGAGTCT
551 GAATTTTATT AGAGCTCACA CACCATATAT TAACATATAC AACTGTGAAC
601 CAGCTAATCC CTCTGAGAAA AACTCCCCAT CTACCCAATA CTGTTACAGC
651 ATACAATCTC TGTTCTTGGG CATTTTGTCA GTGATGCTGA TCTTTGCCTT
701 CTTCCAGGAA CTTGTAATAG CTGGCATCGT TGAGAATGAA TGGAAAAGAA
751 CGTGCTCCAG ACCCAAATCT AACATAGTTC TCCTGTCAGC ACAAGAAAAA
801 AAAGAACAGA CTATTGAAAT AAAAGAAGAA GTGGTTGGGC TAACTGAAAC
851 ATCTTCCCAA CCAAAGAATG AAGAAGACAT TGAAATTATT CCAATCCAAG
901 AAGAGGAAGA AGAAGAAACA GAGACGAACT TTCCAGAACC TCCCCAAGAT
951 CAGGAATCCT CACCAATAGA AAATGACAGC TCTCCTTAAG TGATTTCTTC
1001 TGTTTTCTGT TTCCTTTTTT AAACATTAGT GTTCATAGCT TCCAAGAGAC
1051 ATGCTGACTT TCATTTCTTG AGGTACTCTG CACATACGCA CCACATCTCT

FIG. 13-A

1101 ATCTGGCCTT TGCATGGAGT GACCATAGCT CCTTCTCTCT TACATTGAAT
1151 GTAGAGAATG TAGCCATTGT AGCAGCTTGT GTTGTCACGC TTCTTCTTTT
1201 GAGCAACTTT CTTACACTGA AGAAAGGCAG AATGAGTGCT TCAGAATGTG
1251 ATTCCTACT AACCTGTTCC TTGGATAGGC TTTTATAGTAT AGTATTTTTT
1301 TTTGTCAATTT TCTCCATCAG CAACCAGGGA GACTGCACCT GATGGAAAAG
1351 ATATATGACT GCTTCATGAC ATTCCTAAAC TATCTTTTTT TTATTCCACA
1401 TCTACGTTTT TGGTGGAGTC CCTTTTTATC ATCCTTAAAA CAATGATGCA
1451 AAAGGGCTTT AGAGCACAAT GGATCT

FIG. 13-B

1 CCCAAATGTC TCAGAATGTA TGTCCCAGAA ACCTGTGGCT GCTTCAACCA
 51 TTGACAGTTT TGCTGCTGCT GGCTTCTGCA GACAGTCAAG CTGCAGCTCC
 101 CCCAAAGGCT GTGCTGAAAC TTGAGCCCCC GTGGATCAAC GTGCTCCAGG
 151 AGGACTCTGT GACTCTGACA TGCCAGGGGG CTCGCAGCCC TGAGAGCGAC
 201 TCCATTCACT GGTTCACAA TGGGAATCTC ATTCCCACCC ACACGCAGCC
 251 CAGCTACAGG TTCAAGGCCA ACAACAATGA CAGCGGGGAG TACACGTGCC
 301 AGACTGGCCA GACCAGCCTC AGCGACCCTG TGCATCTGAC TGTGCTTTCC
 351 GAATGGCTGG TGCTCCAGAC CCCTCACCTG GAGTTCCAGG AGGGAGAAAC
 401 CATCATGCTG AGGTGCCACA GCTGGAAGGA CAAGCCTCTG GTCAAGGTCA
 451 CATTCTTCCA GAATGGAAAA TCCCAGAAAT TCTCCCGTTT GGATCCCACC
 501 TTCTCCATCC CACAAGCAAA CCACAGTCAC AGTGGTGATT ACCACTGCAC
 551 AGGAAACATA GGCTACACGC TGTTCTCATC CAAGCCTGTG ACCATCACTG
 601 TCCAAGTGCC CAGCATGGGC AGCTCTTAC CAATGGGGAT CATTGTGGCT
 651 GTGGTCATTG CGACTGCTGT AGCAGCCATT GTTGCTGCTG TAGTGGCCTT
 701 GATCTACTGC AGGAAAAAGC GGATTTACAG CAATTCCACT GATCCTGTGA
 751 AGGCTGCCCC ATTTGAGCCA CCTGGACGTC AAATGATTGC CATCAGAAAG
 801 AGACAACCTG AAGAAACCAA CAATGACTAT GAAACAGCTG ACGGCGGCTA
 851 CATGACTCTG AACCCCAGGG CACCTACTGA CGATGATAAA AACATCTACC
 901 TGACTCTTCC TCCCAACGAC CATGTCAACA GTAATAACTA AAGAGTAACG
 951 TTATGCCATG TGGTCATACT CTCAGCTTGC TGAGTGGATG ACAAAAAGAG
 1001 GGGAAATTGT AAAGGAAAAT TTAAATGGAG ACTGGAAAAA TCCTGAGCAA
 1051 ACAAAACCAC CTGGCCCTTA GAAATAGCTT TAACTTTGCT TAACTACAA
 1101 ACACAAGCAA AACTTCACGG GGTCACTA CATAAAGCA TAAGCAAAAC
 1151 TTAACCTGGA TCATTTCTGG TAAATGCTTA TGTTAGAAAT AAGACAACCC
 1201 CAGCCAATCA CAAGCAGCCT ACTAACATAT AATTAGGTGA CTAGGGACTT
 1251 TCTAAGAAGA TACCTACCCC CAAAAACAA TTATGTAATT GAAAACCAAC
 1301 CGATTGCCTT TATTTTGCTT CCACATTTTC CCAATAAATA CTTGCCTGTG
 1351 ACATTTTGCC ACTGGAACAC TAAACTTCAT GAATTGCGCC TCAGATTTTT
 1401 CCTTTAACAT CTTTTTTTTT TTTGACAGAG TCTCAATCTG TTACCCAGGC
 1451 TGGAGTGCAG TGGTGCTATC TTGGCTCACT GCAAACCCGC CTCCCAGGTT
 1501 TAAGCGATTG TCATGCCTCA GCCTCCCAGT AGCTGGGATT AGAGGCATGT
 1551 GCCATCATAC CCAGCTAATT TTTGTATTTT TTATTTTTTT TTTTGTAGTAG
 1601 AGACAGGGTT TCGCAATGTT GGCCAGGCCG ATCTCGAACT TCTGGCCTCT
 1651 AGCGATCTGC CCGCCTCGGC CTCCCAAAGT GCTGGGATGA CCAGCATCAG

FIG. 14-A

1701 CCCCAATGTC CAGCCTCTTT AACATCTTCT TTCCTATGCC CTCTCTGTGG
1751 ATCCCTACTG CTGGTTTCTG CCTTCTCCAT GCTGAGAACA AAATCACCTA
1801 TTCACTGCTT ATGCAGTCGG AAGCTCCAGA AGAACAAAGA GCCCAATTAC
1851 CAGAACCACA TTAAGTCTCC ATTGTTTTGC CTTGGGATTT GAGAAGAGAA
1901 TTAGAGAGGT GAGGATCTGG TATTCCTGG ACTAAATTCC CCTTGGGGAA
1951 GACGAAGGGA TGCTGCAGTT CCAAAAGAGA AGGACTCTTC CAGAGTCATC
2001 TACCTGAGTC CCAAAGCTCC CTGTCCTGAA AGCCACAGAC AATATGGTCC
2051 CAAATGACTG ACTGCACCTT CTGTGCCTCA GCCGTTCTTG ACATCAAGAA
2101 TCTTCTGTTT CACATCCACA CAGCCAATAC AATTAGTCAA ACCACTGTTA
2151 TTAACAGATG TAGCAACATG AGAAACGCTT ATGTTACAGG TTACATGAGA
2201 GCAATCATGT AAGTCTATAT GACTTCAGAA ATGTTAAAT AGACTAACCT
2251 CTAACAACAA ATTAAAAGTG ATTGTTTCAA GGTGAAAAA

FIG. 14-B

1 GCTGTGACTG CTGTGCTCTG GGCGCCACTC GCTCCAGGGA GTGATGGGAA
 51 TCCTGTGATT CTTACCTGTC CTTGCCACTG AGAGTGACTG GGCTGACTGC
 101 AAGTCCCCC AGCCTTGGGG TCATATGCTT CTGTGGACAG CTGTGCTATC
 151 CCTGGCTCCT GTTGCTGGGA CACCTGCAGC TCCCCAAAG GCTGTGCTGA
 201 AACTCGAGCC CCAGTGGATC AACGTGCTCC AGGAGGACTC TGTGACTCTG
 251 ACATGCCGGG GGA CTCACAG CCCTGAGAGC GACTCCATTG AGTGGTTCCA
 301 CAATGGGAAT CTCATTCCCA CCCACACGCA GCCAGCTAC AGGTTCAAGG
 351 CCAACAACAA TGACAGCGGG GAGTACACGT GCCAGACTGG CCAGACCAGC
 401 CTCAGCGACC CTGTGCATCT GACTGTGCTT TCTGGTCAGT GGAGGAAGGC
 451 CCCAGGGTGG ACCTGGGAGG GCCAGGACGG ATGAAATCTG CTTTCAGGCA
 501 GAGGTTTGCA GGAAAGGGGG GTGGCCTGCT TACTGGGAAG TATCGCTGTG
 551 AGTTGCCTCA GCACATATCA GTGGTTGTTT TTGCCTCAGT TCTGATTGAA
 601 CAGAAGAAGG TTTCAAGGCC AAAACAGGC AGCCAAGTGT GAGAGAAGCA
 651 GAAGGAAATC CCTACTGCAT AAAACCCATT TCCATTTTAA TGGCAGAATT
 701 GAAAAGCACA GACCACAAT GAATCCTAGC CCTGGAAATG ACTCACTATA
 751 CAACATGATG AATTCATTTA ACCCTTGAGT TTCCATTTCT TCACCTGCTC
 801 CGTGGGGCAG TAACGCCTCC CTCAGAGGCT TCTGGTGAGA ATCAGTGTTT
 851 CCCTGCCCCC GCCCGCCCT CCATGCCCTT TCTCCACGTT CTCACTGTGC
 901 TAGGTGCTCT TCTCTGTCTT TCTCTTCCAC CAGCCTGTGG GAAACCTGAG
 951 ATGAAAGTCG TGTCTTACCC ATCTTTGTAT TTCCAGCATC TGAAACTGGG
 1001 CAGAGCTTAA TAAATATTTT GCTGGAGAGG TTGATGATCT TACAAAGCTC
 1051 CCATTGAAAG GTGGCTCTCT GTAAAGCAAA GTTACAATGA GATTGTGATG
 1101 AACATTGTCC TTGTGGCTTT TCACTTAGTC CCCTCCCTTC ACCTGAAGAG
 1151 CAAATTTTCC TCAAAAGTAC ACAGCAAACG AATGACCCAC TGGTGACACT
 1201 GTTGCCCTTA GACCCTGCTG GAAAGAAGCT CCACATTTAT TAACATTCCC
 1251 GAAGTAAATT TATCAGGTAG CATTATCAG GTAACATTTG TTGCACATTC
 1301 ATGACTTTTC TACTGTCCAC AAAGGCATAT GTCCTTATCA TATGCGGACT
 1351 CCTCGGTCAC ACTGGATTCT TCCTTCCCTC CTCGACATGG AAGAGATGGC
 1401 ATCTTAGGGT CTCTTGTTT CTTCTGCAG AGGCCTGTG GGCAGGAAAA
 1451 GGCTGCAGCT GCCTTCCTGG GAGAAGGAGG AGATGAGTGT ATCCTGAACA
 1501 CCTATTATGT GCTAGGGGCT ATTGTAGATA CATGACACTA TCATGCTCAT
 1551 TTTCACGAAT GAGGAACTG AGGCTCAGAA GACTTAAATT ATTTGCCCAA
 1601 GAGTTATAAA TGACAGAGCC AGCATTAGAG TCCAGGACTG TCTGATTTC
 1651 GACCTAAGCT GTTCCCTCTG CACATCGTGT CCCACCAGTA AGGAAGATCT

FIG. 15-A

1701 GGGTCTCAGA GCTGAGCCAA GACCTCCCGG GTCCTCTGCG GTTTTTTTGTG
1751 TCTTTCAGAG TGGCTGGTGC TCCAGACCCC TCACCTGGAG TTCCAGGAGG
1801 GAGAAACCAT CGTGCTGAGG TGCCACAGCT GGAAGGACAA GCCTCTGGTC
1851 AAGGTCACAT TCTTCCAGAA TGGAAAATCC AAGAAATTTT CCCGTTCCGA
1901 TCCCAACTTC TCCATCCCAC AAGCAAACCA CAGTCACAGT GGTGATTACC
1951 ACTGCACAGG AAACATAGGC TACACGCTGT ACTCATCCAA GCCTGTGACC
2001 ATCACTGTCC AAGCTCCCAG CTCTTCACCG ATGGGGATCA TTGTGGCTGT
2051 GGTCACGGG ATTGCTGTAG CGGCCATTGT TGCTGCTGTA GTGGCCTTGA
2101 TCTACTGCAG GAAAAAGCGG ATTTCAAGTT TGTAGCTCCT CCCGGTCCCT
2151 TTTGTTATCA GTTCCACTT T

FIG. 15-B

1 GCCTCGCTCG GCGGCCAGT GGTCTGCGG CCTGGTCTCA CCTCGCCATG
 51 GTTCGTCTGC CTCTGCAGTG CGTCCTCTGG GGCTGCTTGC TGACCGCTGT
 101 CCATCCAGAA CCACCCACTG CATGCAGAGA AAAACAGTAC CTAATAAACA
 151 GTCAGTGCTG TTCTTGTGTC CAGCCAGGAC AGAAACTGGT GAGTGACTGC
 201 ACAGAGTTCA CTGAAACGGA ATGCCTTCCT TGCGGTGAAA GCGAATTCTT
 251 AGACACCTGG AACAGAGAGA CACTGCCA CCAGCACAAA TACTGCGACC
 301 CCAACCTAGG GCTTCGGGTC CAGCAGAAGG GCACCTCAGA AACAGACACC
 351 ATCTGCACCT GTGAAGAAGG CTGGCACTGT ACGAGTGAGG CCTGTGAGAG
 401 CTGTGTCTG CACCGCTCAT GTCGCCCCG CTTTGGGGTC AAGCAGATTG
 451 CTACAGGGGT TTCTGATACC ATCTGCGAGC CCTGCCCAGT CGGCTTCTTC
 501 TCCAATGTGT CATCTGCTTT CGAAAAATGT CACCCTTGA CAAGCTGTGA
 551 GACCAAAGAC CTGGTTGTGC AACAGGCAGGC ACAAACAAGA CTGATGTTGT
 601 CTGTGGTCCC CAGGATCGGC TGAGAGCCCT GGTGGTGATC CCCATCATCT
 651 TCGGGATCCT GTTTGCCATC CTCTTGGTGC TGGTCTTTAT CAAAAAGGTG
 701 GCCAAGAAGC CAACCAATAA GGCCCCCAC CCCAAGCAGG AACCCAGGA
 751 GATCAATTTT CCCGACGATC TTCTGGGCTC CAACACTGCT GCTCCAGTGC
 801 AGGAGACTTT ACATGGATGC CAACCGGTCA CCCAGGAGGA TGGCAAAGAG
 851 AGTCCCATCT CAGTGCAGGA GAGACAGTGA GGCTGCACCC ACCCAGGAGT
 901 GTGGCCACGT GGGCAAACAG GCAGTTGGCC AGAGAGCCTG GTGCTGCTGC
 951 TGCAGGGGTG CAGGCAGAAG CGGGGAGCTA TGCCCACTCA GTGCCAGCCC
 CTC

FIG. 16